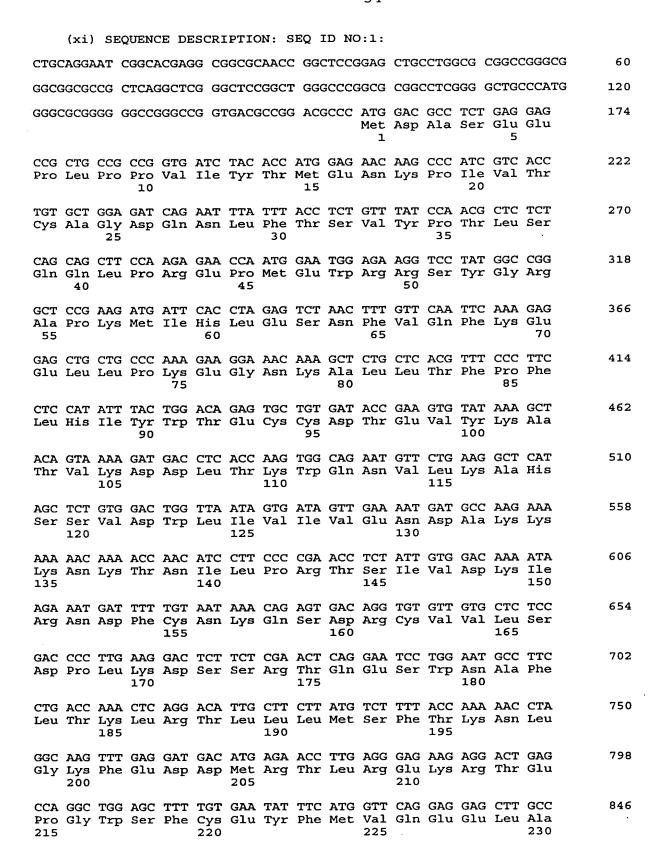
SEQUENCE LISTING

- (1) GENERAL INFORMATION:
 - (i) APPLICANT: Korenberg, Julie R. Yamakawa, Kazuhiro
 - (ii) TITLE OF INVENTION: A NOVEL CHROMOSOME 21 GENE MARKER, COMPOSITIONS AND METHODS USING SAME
 - (iii) NUMBER OF SEQUENCES: 3
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: CAMPBELL & FLORES, LLP
 - (B) STREET: 4370 La Jolla Village Drive, Suite 700
 - (C) CITY: San Diego
 - (D) STATE: California
 - (E) COUNTRY: United States
 - (F) ZIP: 91212
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/337,690
 - (B) FILING DATE: 09-NOV-1994
 - (C) CLASSIFICATION:
 - (viii) ATTORNEY/AGENT INFORMATION:

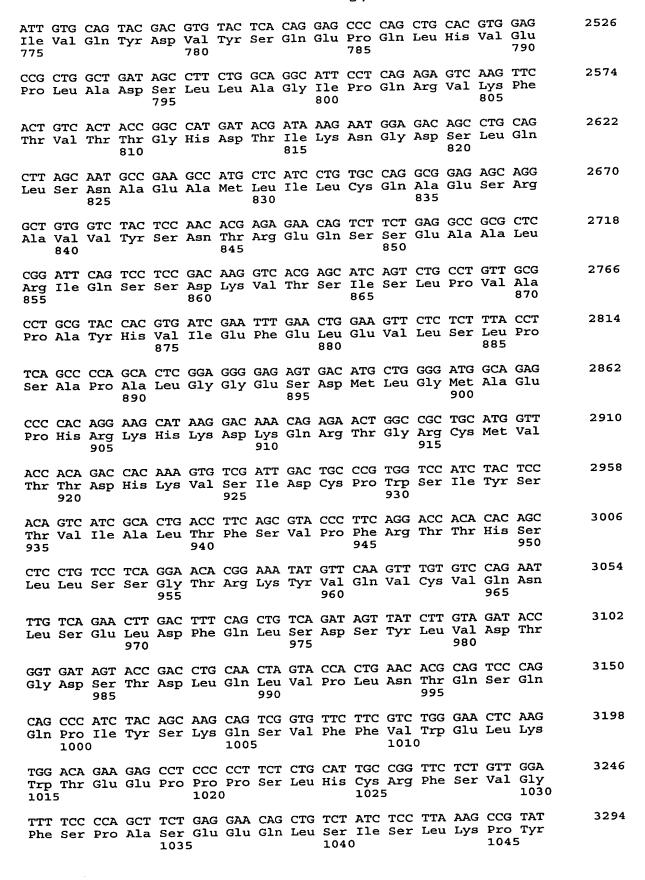
 - (A) NAME: Campbell, Cathryn A.
 (B) REGISTRATION NUMBER: 31,815
 (C) REFERENCE/DOCKET NUMBER: P-CE 2573
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (619)535-9001
 - (B) TELEFAX: (619)535-8949
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5141 base pairs

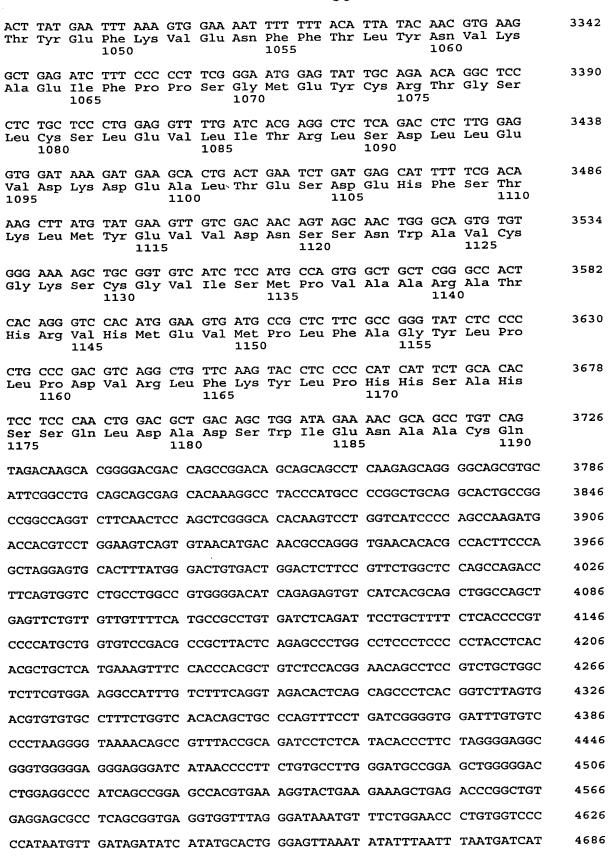
 - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: TRISOMY 21 FETAL BRAIN CDNA LIBRARY
 - (B) CLONE: EHOC-1
 - (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: 21q22.3
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 157..3729

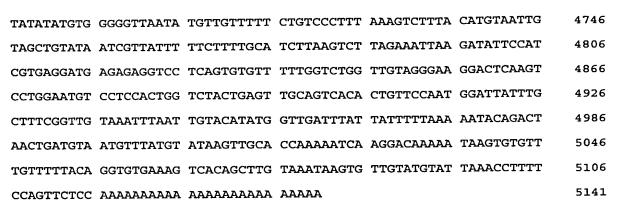


TTT Phe	GTT Val	TTC Phe	GAG Glu	ATG Met 235	CTG Leu	CAG Gln	CAG Gln	TTC Phe	GAG Glu 240	GAC Asp	GCC Ala	CTG Leu	GTG Val	CAG Gln 245	TAC Tyr	894
GAC Asp	GAA Glu	CTG Leu	GAC Asp 250	GCC Ala	CTC Leu	TTC Phe	TCT Ser	CAG Gln 255	TAT Tyr	GTG Val	GTC Val	AAC Asn	TTC Phe 260	GGG Gly	GCC Ala	942
GGG Gly	GAT Asp	GGT Gly 265	GCC Ala	AAC Asn	TGG Trp	CTG Leu	ACT Thr 270	TTT Phe	TTC Phe	TGC Cys	CAG Gln	CCA Pro 275	GTG Val	AAG Lys	AGC Ser	990
TGG Trp	AAC Asn 280	GGA Gly	TTG Leu	ATC Ile	CTC Leu	CGA Arg 285	AAA Lys	CCC Pro	ATA Ile	GAT Asp	ATG Met 290	GAG Glu	AAG Lys	CGG Arg	GAA Glu	1038
TCG Ser 295	ATC Ile	CAG Gln	AGG Arg	CGA Arg	GAA Glu 300	GCC Ala	ACC Thr	CTG Leu	TTA Leu	GAT Asp 305	CTG Leu	CGC Arg	AGT Ser	TAC Tyr	CTG Leu 310	1086
TTC Phe	TCT Ser	CGC Arg	CAG Gln	TGC Cys 315	ACC Thr	TTG Leu	CTG Leu	CTC Leu	TTC Phe 320	CTG Leu	CAG Gln	AGG Arg	CCG Pro	TGG Trp 325	GAG Glu	1134
GTG Val	GCC Ala	CAG Gln	CGC Arg 330	GCC Ala	CTA Leu	GAG Glu	CTG Leu	CTG Leu 335	CAC His	AAC Asn	TGC Cys	GTG Val	CAG Gln 340	GAA Glu	CTG Leu	1182
AAG Lys	CTC Leu	TTA Leu 345	GAA Glu	GTC Val	TCT Ser	GTC Val	CCA Pro 350	CCT Pro	GGT Gly	GCT Ala	CTG Leu	GAC Asp 355	TGC Cys	TGG Trp	GTG Val	1230
TTT Phe	CTG Leu 360	Ser	TGT Cys	CTG Leu	GAG Glu	GTG Val 365	TTG Leu	CAG Gln	AGG Arg	ATA Ile	GAA Glu 370	GGC Gly	TGC Cys	TGT Cys	GAC Asp	1278
CGG Arg 375	Ala	CAG Gln	ATC Ile	GAC Asp	TCA Ser 380	AAC Asn	ATT Ile	GCC Ala	CAC His	ACT Thr 385	GTG Val	GGG Gly	CTA Leu	TGG Trp	AGC Ser 390	1326
TAT Tyr	GCC Ala	ACA Thr	GAA Glu	AAG Lys 395	Leu	AAG Lys	TCC Ser	TTG Leu	GGC Gly 400	TAT Tyr	CTA Leu	TGT Cys	GGA Gly	CTT Leu 405	GTG Val	1374
TCA Ser	GAG Glu	AAA Lys	GGA Gly 410	Pro	AAC Asn	TCA Ser	GAA Glu	GAT Asp 415	Leu	AAC Asn	AGG Arg	ACA Thr	GTT Val 420	Asp	CTT Leu	1422
TTG Leu	GCA Ala	GGT Gly 425	Leu	GGA Gly	GCT Ala	GAG Glu	CGA Arg 430	Pro	GAA Glu	ACA Thr	GCC Ala	AAC Asn 435	Thr	GCT Ala	CAG Gln	1470
AGT Ser	CCT Pro	Туг	Lys	AAA Lys	CTG Leu	AAA Lys 445	Glu	GCA Ala	TTA Leu	TCG Ser	TCA Ser 450	· Val	GAA Glu	GCT Ala	TTT Phe	1518
GAA Glu 455	Lys	CAC His	TAC Tyr	TTA Leu	GAT Asp 460	Leu	TCC Ser	CAT His	GCC Ala	ACC Thr 465	Ile	GAA Glu	ATG Met	TAT Tyr	ACA Thr 470	1566
AGC Ser	ATI	GGG Gly	AGG Arg	ATT	Arg	TCT	GCT Ala	'AAG Lys	TTT Phe 480	Val	GGA Gly	AAA Lys	GAT Asp	CTG Leu 485	GCA Ala	1614
GAG Glu	TTI Phe	TAC Tyr	ATG Met 490	: Arg	L LYS	AAG Lys	GCT Ala	CCA Pro 495	Gln	AAG Lys	GCA Ala	A GAA	ATC 1le 500	туг	CTT Leu	1662

							36				
						GAG Glu					1710
						TGT Cys					1758
						CTC Leu					1806
						TGC Cys 560					1854
						CAT His					1902
						CAT His					1950
						GTT Val					1998
						CAG Gln					2046
						AAG Lys 640					2094
						AAC Asn					2142
	_		_			CCC Pro					2190
_	_	_				TCC Ser		_			2238
						AGA Arg					2286
						CTG Leu 720					2334
						CCA Pro					2382
						ACG Thr					2430
						GTC Val				:	2478







(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1190 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

 (xi)
 SEQUENCE
 DESCRIPTION:
 SEQ ID NO:2:

 Met Asp Ala Ser Glu 1
 Glu Pro Leu Pro Pro Val Ile Tyr Thr Met Glu 15

 Asn Lys Pro Ile Val Thr Cys Ala Gly Asp Gln Asn Leu Phe Thr Ser 25

 Val Tyr Pro Thr Leu Ser Gln Gln Leu Pro Arg Glu Pro Met Glu Trp 45

 Arg Arg Ser Tyr Gly Arg Ala Pro Lys Met Ile His Leu Glu Ser Asn 60

 Phe Val Gln Phe Lys Glu Glu Leu Leu Pro Lys Glu Gly Asn Lys Ala 65

 Leu Leu Thr Phe Pro Rs 85
 Phe Leu His Ile Tyr Trp Thr Glu Cys Cys Asp 95

 Thr Glu Val Tyr Lys Ala Thr Val Lys Asp Asp Leu Thr Lys Trp Gln 100

 Asn Val Leu Lys Ala His Ser Ser Val Asp Trp Leu Ile Val 115

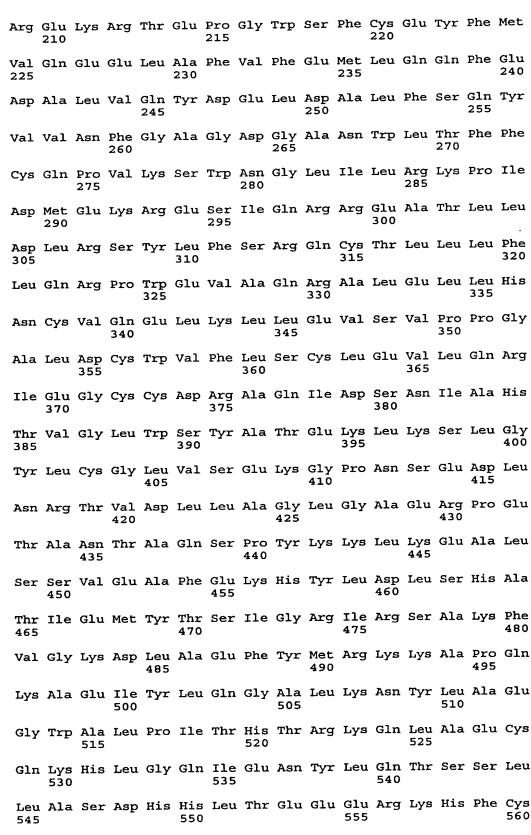
 Glu Asn Asp Ala Lys Lys Lys Asn Lys Thr Asn Ile Leu Pro Arg Thr 130

 Ser Ile Val Asp Lys Ile Arg Asn Asp Phe Cys Asn Lys Gln Ser Asp

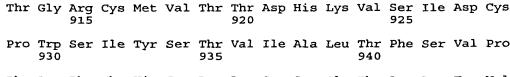
Arg Cys Val Val Leu Ser Asp Pro Leu Lys Asp Ser Ser Arg Thr Gln

Glu Ser Trp Asn Ala Phe Leu Thr Lys Leu Arg Thr Leu Leu Leu Met

Ser Phe Thr Lys Asn Leu Gly Lys Phe Glu Asp Asp Met Arg Thr Leu



Gln Glu Ile Leu Asp Phe Ala Ser Gln Pro Ser Asp Ser Pro Gly His Lys Ile Val Leu Pro Met His Ser Phe Ala Gln Leu Arg Asp Leu His 585 Phe Asp Pro Ser Asn Ala Val Val His Val Gly Gly Val Leu Cys Val 595 600 Glu Ile Thr Met Tyr Ser Gln Met Pro Val Pro Val His Val Glu Gln Ile Val Val Asn Val His Phe Ser Ile Glu Lys Asn Ser Tyr Arg Lys 630 635 Thr Ala Glu Trp Leu Thr Lys His Lys Thr Ser Asn Gly Ile Ile Asn 645 Phe Pro Pro Glu Thr Ala Pro Phe Pro Val Ser Gln Asn Ser Leu Pro Ala Leu Glu Leu Tyr Glu Met Phe Glu Arg Ser Pro Ser Asp Asn Ser Leu Asn Thr Thr Gly Ile Ile Cys Arg Asn Val His Met Leu Leu Arg 695 Arg Gln Glu Ser Ser Ser Leu Glu Met Pro Ser Gly Val Ala Leu Glu Glu Gly Ala His Val Leu Arg Cys Ser His Val Thr Leu Glu Pro 730 Gly Ala Asn Gln Ile Thr Phe Arg Thr Gln Ala Lys Glu Pro Gly Thr Tyr Thr Leu Arg Gln Leu Cys Ala Ser Val Gly Ser Val Trp Phe Val Leu Pro His Ile Tyr Pro Ile Val Gln Tyr Asp Val Tyr Ser Gln Glu Pro Gln Leu His Val Glu Pro Leu Ala Asp Ser Leu Leu Ala Gly Ile Pro Gln Arg Val Lys Phe Thr Val Thr Thr Gly His Asp Thr Ile Lys 805 810 Asn Gly Asp Ser Leu Gln Leu Ser Asn Ala Glu Ala Met Leu Ile Leu Cys Gln Ala Glu Ser Arg Ala Val Val Tyr Ser Asn Thr Arg Glu Gln 840 Ser Ser Glu Ala Ala Leu Arg Ile Gln Ser Ser Asp Lys Val Thr Ser Ile Ser Leu Pro Val Ala Pro Ala Tyr His Val Ile Glu Phe Glu Leu 870 Glu Val Leu Ser Leu Pro Ser Ala Pro Ala Leu Gly Gly Glu Ser Asp 890 Met Leu Gly Met Ala Glu Pro His Arg Lys His Lys Asp Lys Gln Arg 905



Phe Arg Thr Thr His Ser Leu Leu Ser Ser Gly Thr Arg Lys Tyr Val

Gln Val Cys Val Gln Asn Leu Ser Glu Leu Asp Phe Gln Leu Ser Asp 970

Ser Tyr Leu Val Asp Thr Gly Asp Ser Thr Asp Leu Gln Leu Val Pro 980 985

Leu Asn Thr Gln Ser Gln Gln Pro Ile Tyr Ser Lys Gln Ser Val Phe

Phe Val Trp Glu Leu Lys Trp Thr Glu Glu Pro Pro Pro Ser Leu His

Cys Arg Phe Ser Val Gly Phe Ser Pro Ala Ser Glu Glu Gln Leu Ser 1035

Ile Ser Leu Lys Pro Tyr Thr Tyr Glu Phe Lys Val Glu Asn Phe Phe 1050 1045

Thr Leu Tyr Asn Val Lys Ala Glu Ile Phe Pro Pro Ser Gly Met Glu 1060 1065

Tyr Cys Arg Thr Gly Ser Leu Cys Ser Leu Glu Val Leu Ile Thr Arg

Leu Ser Asp Leu Leu Glu Val Asp Lys Asp Glu Ala Leu Thr Glu Ser 1095

Asp Glu His Phe Ser Thr Lys Leu Met Tyr Glu Val Val Asp Asn Ser

Ser Asn Trp Ala Val Cys Gly Lys Ser Cys Gly Val Ile Ser Met Pro 1130 1125 1135

Val Ala Ala Arg Ala Thr His Arg Val His Met Glu Val Met Pro Leu

Phe Ala Gly Tyr Leu Pro Leu Pro Asp Val Arg Leu Phe Lys Tyr Leu 1160

Pro His His Ser Ala His Ser Ser Gln Leu Asp Ala Asp Ser Trp Ile

Glu Asn Ala Ala Cys Gln 1185 1190

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:(A) ORGANISM: Moraxella bovis(C) INDIVIDUAL ISOLATE: MboI linker

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCTGATGCTC GAGTGAATTC

20